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IT IS CLAIMED:

1. A transgenic plant comprising a plant transformation vector comprising a nucleotide sequence that encodes or is complementary to a sequence that encodes a HI0103.1 polypeptide comprising the amino acid sequence of SEQ ID NO:2, or an ortholog thereof, whereby the transgenic plant has a high oil phenotype relative to control plants.

- 2. The transgenic plant of claim 1, which is selected from the group consisting of rapeseed, soy, corn, sunflower, cotton, cocoa, safflower, oil palm, coconut palm, flax, castor and peanut.
- 3. A plant part obtained from the plant according to claim 1.
- 4. The plant part of claim 3, which is a seed.

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- 5. A method of producing oil comprising growing the transgenic plant of claim1 and recovering oil from said plant.
- 6. A method of producing a high oil phenotype in a plant, said method comprising:
- a) introducing into progenitor cells of the plant a plant transformation vector comprising a nucleotide sequence that encodes or is complementary to a sequence that encodes a HI0103.1 polypeptide comprising the amino acid sequence of SEQ ID NO:2, or an ortholog thereof, and
- b) growing the transformed progenitor cells to produce a transgenic plant, wherein
 said polynucleotide sequence is expressed, and said transgenic plant exhibits an altered oil content phenotype relative to control plants.
 - 7. A plant obtained by a method of claim 6.
- 30 8. The plant of claim 7, which is selected from the group consisting of rapeseed, soy, corn, sunflower, cotton, cocoa, safflower, oil palm, coconut palm, flax, castor and peanut.
 - 9. A method of generating a plant having a high oil phenotype comprising identifying a plant that has an allele in its HI0103.1 gene that results in increased oil content compared

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to plants lacking the allele and generating progeny of said identified plant, wherein the generated progeny inherit the allele and have the high oil phenotype.

10. The method of claim 9 that employs candidate gene/QTL methodology.

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11. The method of claim 9 that employs TILLING methodology.